ALIGNMENT 1: SEQ ID NO:7

4.

Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Pig4	1 30 31 60 61 90 91 120 GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCGT CTGGTTACGGTGCTAAAGTTGAAGTATAC GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Pig4	121 150 151 180 181 210 211 240 GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACAACCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT GACGGTGTTGAACTGAATGACAACAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACAACTACTC TTCAACTCCGTATTCCTGGACTTCCTGTT GACGGTGTTGAACTGAAATGACAACAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACAACACTCT TTCAACTCCGGACTTCCTGTGTT ACCGTGTTTGAACTGAAACTAGCAACAACACCAG TTCAAACTGACCATCATCAACTCTAACTCTAAGAATCAGAACTACACAACTACTC TTCAACTCCGGACTTCCTGTGTT ACCGTGTTTCAACTCAGAATCAGAACACACTCTTCCCGTAACTCTTAACTCAACTCAGAATCAGAACACACAC
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	241 270 271 300 301 330 331 330 331 360 TCCTTCTGGATEGCTAATACAGA AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGGATGAATACAGA AACTACGGTTGGAAGATCTCCATCCAGGGTTCCATCCAGGGTTCCATCCA
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	361 390 391 420 421 450 451 480 AACCGTATCATCGATATC AACCGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC AACCGTATCATCTGGACTCTGATGGATATC AACCGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC AACCGTATCATCTGGACTCTGATCGATATC AACCGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC AACCGTATCATCTGGACTCTGATCGATATC AACCGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC AACCGTATCATCGACTCTGATCGATATC AACCGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC
Original_Seg7 Substitute_Seg7 Amended_Seg7 Original_Pig4	481 510 511 540 541 570 571 600 AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCGCTAACGGT GAAATCATCTTCAAACTGGACGGTGACATC AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAACTCTAATACCGACATC AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAACTGAACT
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	601 630 631 720 GATCGTACCCAGTTCATCTGGATGAAATAC TICTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAGACTTCTTCG GATCGTACCCAGTTCATCTGGATGAAATAC TICTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAATAC TICTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAATAC TICTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAATAC TICTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAATAC TICTCCAATATCGAAGAACTGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAATAC TICTCCAATATCGAAGAACGGTTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAATAC TICTCCAATATCGAAGAACGGTTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCAATATCGAAGAACGGTTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAATAC TCTACATCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAATAC TCTTCAATATCGAAGAACGGTTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAATAC TCTTCAATATCGAAGAACGGTTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAATAC TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAATAC TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAATAC TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGATGAATAC TCTTACTCCGAATACCTGAAAGACTTCTGGATGAATACTGAAGACTTCTGGATGAAGACTTCTGGATGAATACTGAAATACTGAAATACTGAAATACTGAAATACTGAATACTGAAATACTGAAATACTGAAATACTGAAATACTGAAATACTGAAATACTGAAATACTGAAATACTGAAATACTGAATACTGAAATACTGAAATACTGAAATACTGAAATACTGAAATACTGAAATACTGAAATACTGAATACTGAAATACTG
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	721 750 751 780 781 810 811 840 GGTAATCCGCTGATGTACAAGAAGTACT TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAGACTCTCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAAGACTCTCCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAAGACTCTCCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC GGTAATCCGGTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAAACAGAAGACTCT TACATCAAACTGAAGAAGACTCTCCCGGTT GGTGAAATCCTGACTCGTTTCCAAATACAAC GGTAAATCAAACACAACAACAACAACAACAACAACAACAACA
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Pig4	841 870 871 900 901 930 931 960 CAGAACTCTAAATACATCACGCGGC CTGTACATCGGTGAAAAGTTCATCATCCGT CGCAAATCTAACTCCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC CAGAACTCTAAATACATCAACTACCGCGAC CTGTACATCGGTGAAAAGTTCATCATCCGT CGCAAATCTAACTCCATCCATGCATGATGAT GACATCGTACGTAAAGAAGACTACATCTAC CAGAACTCTAAATACATCAACTACCGCGAC CTGTACATCGGTGAAAAGTTCATCATCCGT CGCAAATCTAACTCTACGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC CAGAACTCTAAATACATCAACTACCGCGAC CTGTACATCGGTGAAAAGTTCATCATCCGT CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAACACTACATCTAC CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACAGTACA
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	961 990 991 1020 1021 1050 1051 1080 CTIGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACCACCATC CTGGACTTCTTCAACCTGGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC CTGGACTTCTTCAACCTGGAATCAGAATCAGAACACAACACAATC CTGGACTTCTTCAACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC CTGGACTTCTTCAACCTGAACTACAACACACATC CTGGACTTCTTCAACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC CTGGACTTCTTCAACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC CTGGACTTCTTCAACACCTACAAGTACTTCAAGAAAACCTTTCAAGAAAACCTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC CTGGACTTCTTCAACACACAACAACAACACAAC
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	1081 1110 1111 1140 1141 1140 1141 1170 1170
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	1201 1231 1231 1260 1261 1290 1291 1320 GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGGAAGGTTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAAGACGAAGGT GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGGAAGTTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAAGACGAAGGT GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAAGAAGTTAAA CGCAAACCGTACAACTGGATTCC AATTGGCAGTTCATCCCGAAAGACGAAGGT GTATTCGAACAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAAGAGTAAA CGCAAACCGTACAACTGGATTCC AATTGGCAGTTCATCCCGAAAGACGAAGGT GTATTCGAACAATACAAAGACTTACTTCTGC ATCTCCAAATGGTACCTGAAACTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAAGACGAAGGT AATTGGCAGTTCATCCCGAAAGACGTAAAACTGAAACTGGAAACTGGAAACTGGAAGGT AATTGGCAGTTCATCCCGAAAGACGAAGGTAAACTGAAACTGAAACTGGAAACTGGAAACTGAAACTGAAACTGAAACTGAAACTGGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAA
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	1321 1341 TGGACCGAATAGTAAGAATTC TGGACCGAATAGTAAGAATTC TGGACCGAATAGTAAGAATTC TGGACCCAATAGTAAGAATTC

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ALIGNMENT 2: SEQ ID NO:37

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Original_Seq17 Substitute_Seq37 Amended_Seq37 Fig2_*975_App	CTCGAGCCATGGCTCGTCTGCTGTCTACCT CTCGAGCCATGGCTCGTCTGCTGTCTACCT CTCGAGCCATGGCTCGTCTGCTGTCTACCT	TCACTGAATACATCAAGAACATCATCAATA TCACTGAATACATCAAGAACATCATCAATA TCACTGAATACATCAAGAACATCATCAATA TCACTGAATACATCAAGAACATCATCAATA	CCTCCATCCTGAACCTGCGCTACGAATCCA CCTCCATCCTGAACCTGCGCTACGAATCCA CCTCCATCCTGAACCTGCGCTACGAATCCA CCTCCATCCTGAACCTCCGCTACGAATCCA	ATCACCTGATCGACCTGTCTCGCTACGCTT
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	CCAAAATCAACATCGGTTCTAAAGTTAACT CCAAAATCAACATCGGTTCTAAAGTTAACT CCAAAATCAACATCGGTTCTAAAGTTAACT CCAAAATCAACATCGGTTCTAAAGTTAACT	TCGATCCGATCGACAAGAATCAGATCCAGC TCGATCCGATC	TGTTCAATCTGGAATCTTCCAAAATCGAAG TGTTCAATCTGGAATCTTCCAAAATCGAAG TGTTCAATCTGGAATCTTCCAAAATCGAAG TGTTCAATCTGGAATCTTCCAAAATCGAAG	211 240 TTATICCTGAAGAATGCTATICGTATACAACT TTATICCTGAAGAATGCTATICGTATACAACT TTATICCTGAAGAATGCTATICGTATACAACT TTATICCTGAAGAATGCTATICGTATACAACT
Original_Seq37 Substitute_Seq37 Amended_Seq37 Pig2_'975_App	CTATGTACGAAAACTTCTCCACCTCCTTCT CTATGTACGAAAACTTCTCCACCTCCTTCT CTATGTACGAAAACTTCTCCACCTCCTTCT CTATGTACGAAAACTTCTCCACCTCCTTCT	GGATCCGTATCCCTAAATACTTCAACTCCA GGATCCGTATCCCTAAATACTTCAACTCCA	TCTCTCTGAACAATGAATACACCATCATCA TCTCTCTGAACAATGAATACACCATCATCA TCTCTCTGAACAATGAATACACCATCATCA TCTCTCTGAACAATGAATACACCATCATCA	ACTGCATGGAAAACAATTCTGGTTGGAAAG ACTGCATGGAAAACAATTCTGGTTGGAAAG
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	TATCTCTGAACTACGGTGAAATCATCTGGA TATCTCTGAACTACGGTGAAATCATCTGGA	CTCTGCAGGACACTCAGGAAATCAAACAGC CTCTGCAGGACACTCAGGAAATCAAACAGC CTCTGCAGGACACTCAGGAAATCAAACAGC CTCTGCAGGACACTCAGGAAATCAAACAGC	GTGTTGTATTCAAATACTCTCAGATGATCA GTGTTGTATTCAAATACTCTCAGATCATCA GTGTTGTATTCAAATACTCTCAGATGATCA GTGTTGTATTCAAATACTCTCAGATGATCA	ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT
Original_Seq37 Substitute_Seq37 Amended_Seq37 Pig2_'975_App	TCGTTACCATCACCAACAATCGTCTGAATA TCGTTACCATCACCAACAATCGTCTGAATA TCGTTACCATCACCAACAATCGTCTGAATA	ACTCCAAAATCTACATCAACGGCCGTCTGA ACTCCAAAATCTACATCAACGGCCGTCTGA	TCGACCAGAAACCGATCTCCAATCTGGGTA TCGACCAGAAACCGATCTCCAATCTGGGTA TCGACCAGAAACCGATCTCCAATCTGGGTA TCGACCAGAAACCGATCTCCAATCTGGTTA	ACATCCACCOTTCTAATAACATCATGTTCA ACATCCACCOTTCTAATAACATCATGTTCA ACATCCACCOTTCTAATAACATCATGTTCA
Original_Seq17 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	601 630 AACTGGACGGTTGTCGTGACACTCACCGCT AACTGGACGGTTGTCGTGACACTCACCGCT AACTGGACGGTTGTCGTGACACTCACCGCT AACTGGACGGTTGTCGTGACACCTCACCGCT	ACATCTGGATCAAATACTTCAATCTGTTCG ACATCTGGATCAAATACTTCAATCTGTTCG ACATCTGGATCAAATACTTCAATCTGTTCG	ACAAAGAACTGAACGAAAAAGAAATCAAAG ACAAAGAACTGAACGAAAAAGAAATCAAAG ACAAAGAACTGAACGAAAAAGAAATCAAAG ACAAAGAACTGAACGAAAAAGAAATCAAAG	ACCTGTACGACAACCAGTCCAATTCTGGTA ACCTGTACGACAACCAGTCCAATTCTGGTA ACCTGTACGACAACCAGTCCAATTCTGGTA ACCTGTACGACAACCAGTCCAATTCTCGTA
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	721 750 TCCTGANAGACTTCTGGGGTGACTACCTGC TCCTGANAGACTTCTGGGGTGACTACCTGC TCCTGANAGACTTCTGGGGTGACTACCTGC TCCTGANAGACTTCTGGGGTGACTACCTGC	AGTACGACAAACCGTACTACATGCTGAATC AGTACGACAAACCGTACTACATGCTGAATC AGTACGACAAACCGTACTACATGCTGAATC AGTACGACAAACCGTACTACATGCTGAATC	TGTACGATCCGAACAAATACGTTGACGTCA TGTACGATCCGAACAAATACGTTGACGTCA TGTACGATCCGAACAAATACGTTGACGTCA	ACAATGTAGGTATCCGCGGTTACATGTACC ACAATGTAGGTATCCGCGGTTACATGTACC ACAATGTAGGTATCCGCGGTTACATGTACC ACAATGTAGGTATCCGCGGTTACATGTACC
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	841 870 TGAAAGGTCCGCGTGGTTCTGTTATGACTA TGAAAGGTCCGCGTGGTTCTGTTATGACTA TGAAAGGTCCGCCTGGTTCTGTTATGACTA TGAAAGGTCCGCCTGGTTCTGTTATGACTA TGAAAGGTCCGCCTGGTTCTGTTATGACTA	CCAACATCTACCTGAACTCTTCCCTGTACC CCAACATCTACCTGAACTCTTCCCTGTACC CCAACATCTACCTGAACTCTTCCCTGTACC	GTGGTACCAAATTCATCATCAAGAAATACG GTGGTACCAAATTCATCATCAAGAAATACG GTGGTACCAAATTCATCATCAAGAAATACG GTGGTACCAAATTCATCATCAAGAAATACG	CGTCTGGTAACAAGGACAATATEGTTCGCA CGTCTGGTAACAAGGACAATATEGTTCGCA
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	961 ACAATGATCGTGTATACATCAATGTTGTAG ACAATGATCGTGTATACATCAATGTTGTAG ACAATGATCGTGTATACATCAATGTTGTAG ACAATGATCGTGTATACATCAATGTTGTAG ACAATGATCGTGTATACATCAATGTTGTAG	TTAAGAACAAAGAATACCGTCTGGCTACCA TTAAGAACAAAGAATACCGTCTGGCTACCA TTAAGAACAAAGAATACCGTCTGGCTACCA TTAAGAACAAAGAATACCGTCTGGCTACCA	ATGCTTCTCAGGCTGGTGTAGAAAAGATCT ATGCTTCTCAGGCTGGTGTAGAAAAGATCT ATGCTTCTCAGGCTGGTGTAGAAAAGATCT ATGCTTCTCAGGCTGGTGTAGAAAAGATCT	TGTCTGCTCTGGAAATCCCGGACGTTGGTA TGTCTGCTCTGGAAATCCCGGACGTTGGTA TGTCTGCTCTGGAAATCCCGGACGTTGGTA TGTCTGCTCTGGAAATCCCGGACGTTGGTA
Original_Seq37 Substitute_Seq37 Amended_Seq37 Pig2_'975_App	1081 1110 ATCTGTCTCAGGTAGTTGTAATGAAATCCA ATCTGTCTCAGGTAGTTGTAATGAAATCCA ATCTGTCTCAGGTAGTTGTAATGAAATCCA ATCTGTCTCAGGTAGTTGTAATGAAATCCA	AGAACGACCAGGGTATCACTAACAAATGCA AGAACGACCAGGGTATCACTAACAAATGCA AGAACGACCAGGGTATCACTAACAAATGCA AGAACGACCAGGGTATCACTAACAAATGCA	AAATGAATCTGCAGGACAACAATGGTAACG AAATGAATCTGCAGGACAACAATGGTAACG AAATGAATCTGCAGGACAACAATGGTAACG AAATGAATCTGCAGGACAACAATGGTAACG	ATATCGGTTTCATCGGTTTCACCAGTTCA ATATCGGTTTCATCGGTTTCACCAGTTCA ATATCGGTTTCATCGGTTTCACCACTTCA ATATCGGTTTCATCGGTTTCACCACTTCA
Original_Seq17 Substitute_Seq17 Amended_Seq17 Fig2_'975_App	1201 1230 ACANTATOGCTANACTOGTTOCTTCCANCT ACANTATOGCTANACTOGTTOCTTCCANCT ACANTATOGCTANACTOGTTOCTTCCANCT ACANTATOGCTANACTOGTTOCTTCCANCT ACANTATOGCTANACTOGTTOCTTCCANCT ACANTATOGCTANACTOGTTOCTTCANCT	GGTACAATCGTCAGATCGAACGTTCCTCTC GGTACAATCGTCAGATCGAACGTTCCTCTC GGTACAATCGTCAGATCGAACGTTCCTCTC GGTACAATCGTCAGATCGAACGTTCCTCTCTCTCTCTCTC	GCACTCTGGGTTGCTCTTGGGAGTTCATCC GCACTCTGGGTTGCTCTTGGGAGTTCATCC GCACTCTGGGTTGCTCTTTGGGAGTTCATCC	CGGTTGATGACGGTTGGGGTGAACGTCCGC CGGTTGATGACGGTTGGGGTGAACGTCCGC CGGTTGATGACGGTTGGGGTGAACGTCCGC
Original_Seq37 Substitute_Seq37 Amended_Seq37 Pig2_'975_App	1321 1338 TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT			

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ALIGNMENT 3: SEQ ID NO:39

Original_Seq39 Substitute_Seq39 Amended_Seq39 Fig4_'975_App	ATGGCTTTCAACAAATACAATTCCGAAATC ATGGCTTS ECAACAAATACAATTCCGAAATC ATGGCTTTCAACAAATACAATTCCGAAATC ATGGCTTTCAACAAATACAATTCCGAAATC	CTGAACAATATCATCCTGAACCTGCGTTAC CTGAACAATATCATCCTGAACCTGCGTTAC CTGAACAATATCATCCTGAACCTGCGTTAC CTGAACAATATCATCCTGAACCTGCGTTAC	61 90 AAAGACAACAATCTGATCGATCTGCTGGT AAAGACAACAATCTGATCGATCTGCTGGT AAAGACAACAATCTGATCGATCTGCTCTGGT AAAGACAACAATCTGATCGATCTGTCTGGT AAAGACAACAATCTGATCGATCTGTCTGGT	TACGGTGCTAAAGTTGAAGTATACGACGGT TACGGTGCTAAAGTTGAAGTATACGACGGT TACGGTGCTAAAGTTGAAGTATACGACGGT
Original_Seq39 Substitute_Seq39 Amended_Seq39 Fig4_'975_App	GTTGAACTGAATGACAAGAACCAGTTCAAA GTTGAACTGAATGACAAGAACCAGTTCAAA GTTGAACTGAATGACAAGAACCAGTTCAAA GTTGAACTGAATGACAAGAACCAGTTCAAA	CTGACCTCTTCCGCTAACTCTAAGATCCGT CTGACCTCTTCCGCTAACTCTAAGATCCGT CTGACCTCTTCCGCTAACTCTAAGATCCGT CTGACCTCTTCCGCTAACTCTAAGATCCGT	181 210 GTTACTCAGAATCAGAACATCATCTTCAAC GTTACTCAGAATCAGAACATCATCTTCAAC GTTACTCAGAATCAGAACATCATCTTCAAC GTTACTCAGAATCAGAACATCATCTTCAAC	TCCGTATTCCTGGACTTCTCTGTTTCCTTC TCCGTATTCCTGGACTTCTCTGTTTCCTTC TCCGTATTCCTGGACTTCTCTTTTCTTT
Original_Seq39 Substitute_Seq39 Amended_Seq39 Pig4_'975_App	TGGATCCGTATCCCGAAATACAAGAACGAC TGGATCCGTATCCCGAAATACAAGAACGAC TGGATCCGTATCCCGAAATACAAGAACGAC	GGTATCCAGAATTACATCCACAATGAATAC GGTATCCAGAATTACATCCACAATGAATAC GGTATCCAGAATTACATCCACAATGAATAC GGTATCCAGAATTACATCCACAATGAATAC	ACCATCATCAACTGCATGAAGAATAACTCT ACCATCATCAACTGCATGAAGAATAACTCT ACCATCATCAACTGCATGAAGAATAACTCT ACCATCATCAACTGCATGAAGAATAACTCT	GGTTGGAAGATCTCCATCCGCGGTAACCGT GGTTGGAAGATCTCCATCCGCGGTAACCGT GGTTGGAAGATCTCCATCCGCGGTAACCGT
Original_Seq39 Substitute_Seq39 Amended_Seq39 Pig4_'975_App	ATCATCTGGACTCTGATCGATATCAACGGT ATCATCTGGACTCTGATCGATATCAACGGT ATCATCTGGACTCTGATCGATATCAACGGT	AAGACCAAATCTGTATTCTTCGAATACAAC AAGACCAAATCTGTATTCTTTCGAATACAAC AAGACCAAATCTGTATTCTTCGAATACAAC AAGACCAAATCTGTATTCTTTCGAATACAAC	421 450 ATCCGTGAAGACATCTCTGAATACATCAAT ATCCGTGAAGACATCTCTGAATACATCAAT ATCCGTGAAGACATCTCTGAATACATCAAT ATCCGTGAAGACATCTCTGAATACATCAAT ATCCGTGAAGACATCTCTGAATACATCAAT	CGCTGGTTCTTCGTTACCATCACCAATAAC CGCTGGTTCTTCGTTACCATCACCAATAAC CGCTGGTTCTTCGTTACCATCACCAATAAC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Pig4_'975_App	CTGAACAATGCTAAAATCTACATCAACGGT CTGAACAATGCTAAAATCTACATCAACGGT CTGAACAATGCTAAAATCTACATCAACGGT	AAACTGGAATCTAATACCGACATCAAAGAC AAACTGGAATCTAATACCGACATCAAAGAC AAACTGGAATCTAATACCGACATCAAAGAC AAACTGGAATCTAATACCGACATCAAAGAC	541 570 ATCCGTGAAGTTATCGCTAACGGTGAAATC ATCCGTGAAGTTATCGCTAACGGTGAAATC ATCCGTGAAGTTATCGCTAACGGTGAAATC ATCCGTGAAGTTATCGCTAACGGTGAAATC	ATCTTCAAACTGGACGGTGACATCGATCGT ATCTTCAAACTGGACGGTGACATCGATCGT ATCTTCAAACTGGACGGTGACATCGATCGT
Original_Seq39 Substitute_Seq39 Amended_Seq39 Fig4_'975_App	ACCCAGTTCATCTGGATGAAATACTTCTCC	ATCTTCAACACCGAACTGTCTCAGTCCAAT ATCTTCAACACCGAACTGTCTCAGTCCAAT ATCTTCAACACCGAACTGTCTCAGTCCAAT ATCTTCAACACCGAACTGTCTCAGTCCAAT	ATCGAAGAACGGTACAAGATCCAGTCTTAC ATCGAAGAACGGTACAAGATCCAGTCTTAC ATCGAAGAACGGTACAAGATCCAGTCTTAC ATCCAAGAACAGAAC	TCCGAATACCTGAAAGACTTCTGGGGTAAT TCCGAATACCTGAAAGACTTCTGGGGTAAT TCCGAATACCTGAAAGACTTCTGGGGTAAT
Original_Seq39 Substitute_Seq39 Amended_Seq39 Pig4_'975_App	750 CCGCTGATGTACAACAAAGAATACTATATG CCGCTGATGTACAACAAAGAATACTATATG CCGCTGATGTACAACAAAGAATACTATATG CCGCTGATGTACAACAAAGAATACTATATG	TTCAATGCTGGTAACAAGAACTCTTACATC TTCAATGCTGGTAACAAGAACTCTTACATC TTCAATGCTGGTAACAAGAACTCTTACATC TTCAATGCTGGTAACAAGAACTCTTACATC	AAACTGAAGAAAGACTCTCCGGTTGGTGAA AAACTGAAGAAAGACTCTCCGGTTGGTGAA AAACTGAAGAAAGACTCTCCGGTTGGTGAA AAACTGAAGAAGACTCTCCCGGTTGGTGAA	STCCTGACTCGTTCCAAATACAACCAGAAC TCCTGACTCGTTCCAAATACAACCAGAAC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Fig4_'975_App	841 TCTAAATACATCAACTACCGCGACCTGTAC TCTAAATACATCAACTACCGCGACCTGTAC TCTAAATACATCAACTACCGCGACCTGTAC TCTAAATACATCAACTACCGCGACCTGTAC TCTAAATACATCAACTACCGCGACCTGTAC	ATCGGTGAAAAGTTCATCATCGGTCGCAAA ATCGGTGAAAAGTTCATCATCGGTCGCAAA ATCGGTGAAAAGTTCATCATCCGTCGCAAA ATCGGTGAAAAGTTCATCATCATCGTAAA	TCTAACTCTCAGTCCATCAATGAGGACATC TCTAACTCTCAGTCCATCAATGATGACATC TCTAACTCTCAGTCCATCAATGATGACATC	GTACGTAAAGAAGACTACATCTACCTGGAC GTACGTAAAGAAGACTACATCTACCTGGAC GTACGTAAAGAAGACTACATCTACCTGGAC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Fig4_'975_App	961 PICTICAACCTGAATCAGTAATGGCGTGTA TICTICAACCTGAATCAGGAATGGCGTGTA TICTICAACCTGAATCAGGAATGGCGTGTA TICTICAACCTGAATCAGGAATGGCGTGTA TICTICAACCTGAATCAGGAATGGCGTGTA	TACACCTACAAGTACTTCAAGAAAGAAGAA TACACCTACAAGTACTTCAAGAAAGAAGAA TACACCTACAAGTACTTCAAGAAAGAAGAA TACACCTACAAGTACTTCAAGAAAGAAGAA	GAAAAGCTTTTCCTGGCTCCGATCTCTGAT GAAAAGCTTTTCCTGGCTCCGATCTCTGAT GAAAAGCTTTTCCTGGCTCCGATCTCTGAT	TCCGACGAACTCTACAACACCATCCAGATC TCCGACGAACTCTACAACACCATCCAGATC TCCGACGAACTCTACAACACCATCCAGATC TCCGACGAACTCTACAACACCATCCAGATC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Pig4_'975_App	1081 1110 AAAGAATACGACGAACAGCCGACCTACTCT AAAGAATACGACGAACAGCCGACCTACTCT AAAGAATACGACGAACAGCCGACCTACTCT AAAGAATACGACGAACAGCCGACCTACTCT AAAGAATACGACGAACAGCCGACCTACTCT AAAGAATACGACGAACAGCCGACCTACTCT	TGCCAGCTGCTGTTCAAGAAAGATGAAGAA TGCCAGCTGCTGTTCAAGAAAGATGAAGAA TGCCAGCTGCTGTTCAAGAAAGATGAAGAA TGCCAGCTGCTGTTCAAGAAAGATGAAGAA	TCTACTGACGAAATCGGTCTGATCGGTATC TCTACTGACGAAATCGGTCTGATCGGTATC TCTACTGACGAAATCGGTCTGATCGGTATC	CACCGTTTCTACGAATCTGGTATCGTATTC CACCGTTTCTACGAATCTGGTATCGTATTC CACCGTTTCTACGAATCTGGTATCGTATTC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Fig4_'975_App	1201 1230 1 GAAGAATACAAAGACTTCTTCTGCATCTCC 2 GAAGAATACAAAGACTTCTTCTTGCATCTCC 2 GAAGAATACAAAGACTTCTTCTGCATCTCC 2 GAAGAATACAAAGACTTCTTCTGCATCTCC 2	AAATGGTACCTGAAGGAAGTTAAACGCAAA AAATGGTACCTGAAGGAAGTTAAACGCAAA AAATGGTACCTGAAGGAAGTTAAACGCAAA AAATGGTACCTGAAGGAAGTTAAACGCAAA	CCGTACAACCTGAAACTGGGTTGCAATTGG CCGTACAACCTGAAACTGGGTTGCAATTGG CCGTACAACCTGAAACTGGGTTGCAATTGG	AGTTCATCCCGAAAGACGAAGGTTGGACC AGTTCATCCCGAAAGACGAAGGTTGGACC AGTTCATCCCGAAAGACGAAGGTTGGACC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Pig4_'975_App	1321 1350 1 GAATAGTAACCTCTAGAGTCGAGGCCTGCA C GAATAGTAACCTCTAGAGTCGAGGCCTGCA C GAATAGTAACCTCTAGAGTCGAGGCCTGCA C GAATAGTAACCTCTAGAGTCGAGGCCTGCA C			

ALIGNMENT 4: SEQ ID NO:40

Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186				91 120
			***************************************	TMIKLPNRIKSKPLGEKLLEMIINGIPYLG
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186		••••••		211 240 GASIFNRRGYFSDPALILMHELIHVLHGLY
MIGTAIL_MOTITO				
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186	***************************************	TFGGQDPSIITPSTDKSIYDKVLQNFRGIV		331 360 VEDSEGKYSIDVESFDKLYKSLMPGPTETN
Original_Seq40	361 390	391 420	421 450	451 480
Substitute_Seq40 Amended_Seq40 Whelan_M81186				NEDLPPIADKNSPSDDLSKNERIEYNTQSN
Original_Seq40 Substitute_Seq40	481 510	511 540	541 570	571 600
Amended_Seq40 Whelan_M81186	YIENDFPINELILDTDLISKIELPSENTES	LTDPNVDVPVYEKQPAIKKIPTDENTIPQY	LYSQTFPLDIRDISLTSSPDDALLFSNKVY	SPFSMDYIKTANKVVEAGLFAGWVKQIVND
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186		631 660 GNETAKGNPENAPEIAGASILLEPIPELLI		
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186				
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186	841 870	871 900 KDNNL I DLSGYGAKVEVYDGVELNDKNOFK KDNNL I DLSGYGAKVEVYDGVELNDKNOPK	901 930 LTSSANSKIRVTONONIIFNSVFLDFSVSP LTSSANSKIRVTONONIIFNSVFLDFSVSP LTSSANSKIRVTONONIIFNSVFLDFSVSP LTSSANSKIRVTONONIIFNSVFLDFSVSP	WIRIPKYKNDGIQNYIHNBYTIINCMKNNS WIRIPKYKNDGIQNYIHNBYTIINCMKNNS WIRIPKYKNDGIQNYIHNBYTIINCMKNNS
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186	GWKISIRGNRIEWTLIDINGKTKSVPFEYN GWKISIRGNRIEWTLIDINGKTKSVPFEYN	991 1020 IREDISEYINRWPPVTITNNINNAKIYING IREDISEYINRWPPVTITNNINNAKIYING IREDISEYINRWPPVTITNNINNAKIYING IREDISEYINRWPPVTITNNINNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGDIDR KLESNTDIKDIREVIANGEIIFKLDGDIDR KLESNTDIKDIREVIANGEIIFKLDGDIDR KLESNTDIKDIREVIANGEIIFKLDGDIDR	TQFIWMKYPSIFNTELSQSNIBERYKIQSY TQFIWMKYPSIFNTELSQSNIBERYKIQSY TQFIWMKYPSIFNTELSQSNIBERYKIQSY
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186	SEYLKDPWGNPLMYNKEYYMPNAGNKNSY I	KLKKDSPYGEILTRSKYNONSKYINYRDLY KLKKDSPYGEILTRSKYNONSKYINYRDLY KLKKDSPYGEILTRSKYNONSKYINYRDLY KLKKDSPYGRILTRSKYNONSKYINYRDLY	IGEKFIIRRKSNSQSINDDIVRKEDYIYLD IGEKFIIRRKSNSQSINDDIVRKEDYIYLD IGEKFIIRRKSNSQSINDDIVRKEDYIYLD IGEKFIIRRKSNSQSINDDIVRKEDYIYLD	FFNLNGERVYTYKEPKKEEEKLPLAPISD FFNLNGERVYTYKYPKKEEEKLPLAPISD FFNLNGERVYTYKYFKKEEEKLPLAPISD
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186	1201 1230 SDEPYNTIQIKEYDEQPTYSCOLLPKKDEE SDEPYNTIQIKEYDEQPTYSCOLLPKKDEE SDEPYNTIQIKEYDEQPTYSCOLLPKKDEE SDEPYNTIQIKEYDEQPTYSCOLLPKKDEE	STDEIGLIGIHRFYESGIVFEEYKDYPCIS STDEIGLIGIHRFYESGIVFEEYKDYPCIS STDEIGLIGIHRFYESGIVFEEYKDYPCIS STDEIGLIGIHRFYESGIVFEEYKDYPCIS	KWYLKEVKRKPYNLKLGCNWOFIPKDEGWT KWYLKEVKRKPYNLKLGCNWOFIPKDEGWT KWYLKEVKRKPYNLKLGCNWOFIPKDEGWT	E E E

ALIGNMENT 5: SEQ ID NO:41

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Original_Seq41 Substitute_Seq41	1 30		61 90	91 120
Amended_Seq41 Thompson_X52066	MÕEANKÕENÄKDBANGADIVÄIKI BNAGÖW	QPVKAPKIHNKIWVIPERDTPTNPEEGDLN	PPPEAKQVPVSYYDSTYLSTDNEKDNYLKG	VTKLFER IYSTDLGRMLLTS I VRG I PFWGG
Original_Seq41 Substitute_Seq41		151 180	181 210	211 240
Amended_Seq41 Thompson_X52066	STIDTELKVIDTNCINVIQPDGSYRSEELN	LVIIGPSADIIQPECKSPGHEVLNLTRNGY	GSTQYIRFSPDFTFGFEESLEVDTNPLLGA	GKPATDPAVTLAHELIHAGHRLYGIAINPN
Original_Seq41 Substitute_Seq41 Amended Seq41	***************************************	271 300	301 330	331 360
Thompson_X52066	RVFKVNTNAYYEMSGLEVSFEELRTFGGHD	akpidsloeneprlyyynkpkdiastlnka	KSIVGTTASLQYNKNVFKEKYLLSEDTSGK	FSVDKLKFDKLYKMLTE (YTEDNPVKPPKV
Original_Seq41 Substitute_Seq41 Amended Seq41			421 450AL	451 480 NDLCI KVNNWDLFFSPSEDNFTNDLNKGEE NDLCI KVNNWDLFFSPSEDNFTNDLNKGEE NDLCI KVNNWDLFSPSSEDNFTNDL NKGEE
Thompson_X52066	LNRKTYLNPDKAVPKINIVPKVNYTIYDGP	nlrntnlaanfngonte i nimnftkl knft	GLFEFYKLLCVRGIITSKTKSLDKGYNKAL	NDLCIKVNNWDLPFSPSEDNFTNDLNKGEE
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066	ITSDTNIEAAEENISLDLIQQYYLTFNFDN ITSDTNIEAAEENISLDLIQQYYLTFNFDN ITSDTNIEAAEENISLDLIQQYYLTFNFDN	EPENISIENLSSDIIGQLELMPNIERPPNG EPENISIENLSSDIIGQLELMPNIERPPNG EPENISIENLSSDIIGQLELMPNIERPPNG EPENISIENLSSDIIGQLELMPNIERPPNG	541 570 KKYELDKYTMPHYLRAQEFEHGKSRIALTN KKYELDKYTMPHYLRAQEFEHGKSRIALTN KKYELDKYTMPHYLRAQEFEHGKSRIALTN KKYELDKYTMPHYLRAQEFEHGKSRIALTN	SVNEALLNPSRVYTPFSSDYVKKVNKATEA SVNEALLNPSRVYTPFSSDYVKKVNKATEA SVNEALLNPSRVYTPPSSDYVKKVNKATEA
Original_Seg41 Substitute_Seg41 Amended_Seg41 Thompson_X52066	AMPLGWVEULVYDFTDETSEVSTTDKIADI	TIIIPYIGPALNIG MLYKDDFVGALIFSG TIIIPYIGPALNIG MLYKDDFVGALIFSG TIIIPYIGPALNIG MLYKDDFVGALIFSG TIIIPYIGPALNIG MLYKDDFVGALIFSG	661 690 AVILLEFIPEIAIPVLGTFALVSYIANKVL AVILLEFIPEIAIPVLGTFALVSYIANKVL AVILLEFIPEIAIPVLGTFALVSYIANKVL AVILLEFIPEIAIPVLGTFALVSYIANKVL	TVQTIDNALSKRNEKWDEVYKYIVTNWLAK TVQTIDNALSKRNEKWDEVYKYIVTNWLAK TVQTIDNALSKRNEKWDEVYKYIVTNWLAK TVQTIDNALSKRNEKWDEVKYYIVTNWLAK
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066	VNTQIDLIRKMKEALENQAEATKAIINYQ VNTQIDLIRKMKEALENQAEATKAIINYQ VNTQIDLIRKMKEALENQAEATKAIINYQ	YNQYTEEEKNNINFNIDDLSSKLINESINKA YNQYTEEEKNNINFNIDDLSSKLINESINKA YNQYTEEEKNNINFNIDDLSSKLINESINKA YNQYTEEEKNNINFNIDDLSSKLINESINKA	781 MININKPLNQCSVSYLMNSMIPYGVKRLED MININKPLNQCSVSYLMNSMIPYGVKRLED MININKPLNQCSVSYLMNSMIPYGVKRLED MININKPLNQCSVSYLMNSMIPYGVKRLED	FDASLKDALLKYINDNYGTLIGOVDRLKDK PDASLKDALLKYINDNYGTLIGOVDRLKDK FDASLKDALLKYINDNYGTLIGOVDRLKDK
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066	841 870 VNNTLSTDIPFOLSKYVDNORLLSTFTEYI VNNTLSTDIPFOLSKYVDNORLLSTFTEYI VNNTLSTDIPFOLSKYVDNORLLSTFTEYI VNNTLSTDIPFOLSKYVDNORLLSTFTEYI VNNTLSTDIPFOLSKYVDNORLLSTFTEYI	KNI INTS ILNLRYESNHLIDLSRYASKINI KNI INTS ILNLRYESNHLIDLSRYASKINI KNI INTS ILNLRYESNHLIDLSRYASKINI KNI INTS ILNLRYESNHLIDLSRYASKINI	GSKVNPDPIDKNQIQLPNLESSKIEVILKN GSKVNPDPIDKNQIQLPNLESSKIEVILKN GSKVNPDPIDKNQIQLPNLESSKIEVILKN	AIVYNSMYENPSTSPWIRIPKYPNSISLNN AIVYNSMYENPSTSPWIRIPKYPNSISLNN AIVYNSMYENPSTSPWIRIPKYPNSISLNN
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066	961 EYTI INCMENNSGWKVSLNYGE I WTLQDT EYTI INCMENNSGWKVSLNYGE I WTLQDT EYTI I NCMENNSGWKVSLNYGE I WTLQDT EYTI I NCMENNSGWKVSLNYGE I WTLQDT EYTI I NCMENNSGWKVSLNYGE I WTLQDT	QEIKQRVVFKYSQMINISDYINRWIFVTIT QEIKQRVVFKYSQMINISDYINRWIFVTIT QEIKQRVVFKYSQMINISDYINRWIFVTIT QEIKQRVVFKYSQMINISDYINRWIFVTIT	NNRLNNSKIY II INGRLIDQKPISNLGNIHA NNRLNNSKIY II INGRLIDQKPISNLGNIHA NNRLNNSKIY II INGRLIDQKPISNLGNIHA NNBLNNSKIY II INGRLIDQKPISNLGNIGNIHA	SNN IMFKLDGCRDTHRY IWI KYPNLPDKEL SNN IMFKLDGCRDTHRY IWI KYPNLPDKEL SNN IMFKLDGCRDTHRY IWI KYPNLPDKEL
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066	1081 1110 NEKEIKDLYDNOSNSGILKDFWGDYLQYDK NEKEIKDLYDNOSNSGILKDFWGDYLQYDK NEKEIKDLYDNOSNSGILKDFWGDYLQYDK NEKEIKDLYDNOSNSGILKDFWGDYLQYDK	PYYMITLYDPNKYVDVNNVGIRGYMYLKGP PYYMITLYDPNKYVDVNNVGIRGYMYLKGP PYYMINLYDPNKYVDVNNVGIRGYMYLKGP	rgsvmttniylnsslyrgtkfiikkäasgn rgsvmttniylnsslyrgtkfiikkvasgn rgsvmttniylnsslyrgtkfiikkvasgn	KDN I VRNNDRVY I NVVVKNKEYRLATNASQ KDN I VRNNDRVY I NVVVKNKEYRLATNASQ KDN I VRNNDRVY I NVVVKNKEYRLATNASQ
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066	1201 1230 AGVEKILSALEIPDVGNLSQVVVMKSKNDQ AGVEKILSALEIPDVGNLSQVVVMKSKNDQ AGVEKILSALEIPDVGNLSQVVVMKSKNDQ AGVEKILSALEIPDVGNLSQVVVMKSKNDQ	GITNKCKMNLQDNNGNDIGFIGFHQFNNIA GITNKCKMNLQDNNGNDIGFIGFHQFNNIA GITNKCKMNLQDNNGNDIGFIGFHQFNNIA GITNKCKMNLQDNNGNDIGFIGFHOFNNIA	KLVASNWYN RIERSSRTLGCSWEF I PVDD KLVASNWYN ROTERSSRTLGCSWEF I PVDD KLVASNWYN ROJERSSRTLGCSWEF I PVDD KLVASNWYN ROJERSSRTLGCSWEF I PVDD KLVASNWYN ROJERSSRTLGCSWEF I PVDD	GWGERPL GWGERPL GWGRR DI

ALIGNMENT 6: SEQ ID NO:42

				
	1 30	31 60	61 90	91 120
Original_Seq42				72 120
Substitute_Seq42				***************************************
Amended_Seq42				
Whelan M81186	MPVT INNFNYNDP I DNNN I IMMEPPFARGT	GRYYKAFKITORIWIIPERYTFGYKPEDPN	KSSGIPNROVCEYYDPDYLNINDKKNIPLO	TMIKLPHRIKSKPLGEKLLEMIINGIPYLG
	121 150	151 180	181 210	211 240
Original_Seq42				
Substitute_Seq42		***************************************		
Amended_Seq42				
Whelan_M81186	DRRVPLEEFNTN I ASVTVNKL I SNPGEVER	KKGIFANLIIFGPGPVLNENETIDIGIQNH	FASREGFGGIMQMKFCPEYVSVFNNVQENK	GASIFNRRGYFSDPALILMHELIHVLHGLY
	241 270	271 300	301 330	331 360
Original_Seq42	***	2,1	301 330	331 300
Substitute Seq42			***************************************	
Amended Seq42			***************************************	
Whelan_M81186	GIKVDDLPIVPNEKKFFMQSTDAIQAEELY	TFGGQDPS I ITPSTDKS IYDKVLQNPRGIV	DRLNKVLVCISDPNININIYKNKPKDKYKF	VEDSEGKYSIDVESPDKLYKSLMFGFTETN
	363			
Original_Seq42	361 390	391 420	431 450 APGICIDVD	451 480
Substitute_Seq42			A DOTOTOM	NEDT BET BOWNEDCODY CONTERT PROSPECT
Amended Seq42		***************************************	APGICIDVD	MEDITEL THOMAS CONDUCTION IN INTERNATION
Whelan_M81186	IABNYKIKTRASYFSDSLPPVKIKNLLDNE	IYTIEEGFNI SDKDMEKEYRGONKA INKOA	YEEISKEHLAVYKIQMCKSVKAPGICIDVD	NEDLEF LADKING PODDLSKNER LEVITORN
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	481 510		541 570	571 600
Original_Seq42	YIENDPPINELILDTDLISKIELPSENTES	LTDPNVDVPVYEKQPAIKKIFTDENTIFQY	LYSQTFPLDIRDISLTSSFDDALLPSNKVY	SFFSMDYIKTANKVVEAGLFAGWVKQIVND
Substitute_Seq42	YIENDFPINELILDTDLISKIELPSENTES	LTDFNVDVPVYEKQPA I KK I PTDENT I FQY	LYSQTPPLDIRDISLTSSFDDALLFSNKVY	SPFSMDYIKTANKVVEAGLFAGWVK0IVND
Amended_Seq42	YIENDFPINELILDTDLISKIELPSENTES	LTDFNVDVPVYEKQPAIKKIFTDENTIFQY	LYSQTFPLDIRDISLTSSFDDALLFSNKVY	SFPSMDYIKTANKVVEAGLPAGWVKQIVND
Whelan_M81186	TIENDFPINELILDIDLISKIELPSENTES	LIDFNVDVPVYEKQPAIKKIFIDENTIPQY	LYSQTFPLDIRDISLTSSFDDALLFSNKVY	SFFSMDYIKTANKVVEAGLPAGWVKQIVND
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	601 630	631 660	661 690	691 720
Original_Seq42	FVIEANKSNTMDKIADISLIVPYIGLALNV	GNETAKGNPENAPEIAGASILLEPIPELLI	PVVGAFLLESYIDNKNKIIKTIDNALTKRN	EKWSDMYGLIVAOWLSTVNTOFYTIKEGNY
Substitute_Seq42	FVIEANKSNTMDKIADISLIVPYIGLALNV	GNETAKGNPENAPEIAGASILLEFIPELLI	PVVGAFLLESYIDNKNKI I KTIDNALTKRN	EKWSDMYGLIVAOWLSTVNTOFYTIKEGMY
Amended_Seq42	PVIEANKSNIMDKIADISLIVPYIGLALNV	GNETAKGNFENAPEIAGASILLEFIPELLI	PVVGAFLLESYIDNKNKI I KTIDNALTKRN	EXWSDMYGLIVAOWLSTVNTOFYTIKEGMY
Whelan_M81186	FVIEANKSNTMDKIADISLIVPYIGLALNV	GNETAKGNFENAFEIAGASILLEFIPELLI	PVVGAFLLESYIDNKNK1 IKTIDNALTKRN	EKWSDMYGLIVAQWLSTVNTQFYTIKEGMY
	721 750	751 780	701	
Original_Seq42			SYLMKKMI PLAVEKLLDFDNTLKKNLLNYI	811 840
Substitute_Seq42	KALNYQAQALEEIIKYRYNIYSEKEKSNIN	IDENDINSKLNEGINGAIDNINNFINGCSV	SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI	DENKT VI. I CCAEVEKEKUNKYI KTIMBEDI
Amended_Seq42	KALNYQAQALEEI I KYRYNI YSEKEKSNIN	IDFNDINSKLNEGINOAIDNINNFINGCSV	SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI	DENKLYLICSARYEKSKVNKYLKTIMPPOL
Whelan_M81186	KALNYOAOALEEIIKYRYNIYSEKEKSNIN	IDENDINSKINEGINGA IDNINNFINGCSV	SVIMERMI DI AVEKI I DEDMEN KEMI I MVI	DENVI VI TECKOVOVEVINIVVI VETMODOT
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Original_Seg42	841 870	871 900	930	931 960
Substitute Seq42	CIVENITY I DEPRENDED IN THE SU	KDNNE I DE GOVERNOUS KENNENDEN IN INCHES	LTSSANSKIRMTQNQNIIPNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Amended Seg42	SIYTNDTILIEMFNKYNSEILNNIILNLRY SIYTNDTILIEMFNKYNSEILNNIILNLRY SIYTNDTILIEMFNKYNSEILNNIILNLRY	KDMMI 1D1 CGAC PRINCIAL DOMEST MANUAL KDMMI 1D1 CGAC PRINCIAL ADARDA MANUAL MAN	LTSSANSKIRMTONONI I FNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Whelan M81186	SIYTNDTILIEMFNKYNSEILNNIILNIRY	KDNNI.IDI.SGYGAKVEVIDGVELNDKNOPK	LTSSANSKIR TONONIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
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Original_Seq42	GWKISIRG RIIWTLIDINGKTKSVFFEYN	IREDISEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGDIDR	TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Substitute_Seq42 Amended_Seq42	GWK1S1RGNR11WTLIDINGKTKSVPFEYN	IREDISEYINDWFFVTITNNINNAKIYING	KI.ESMTDIKDIPEVIANCETIEVIACOTOR	TODIUMEVOCI PAPPOI COCAL CODVETOCA
Whelan_M81186	CHAIGIRGUALIMITIDINGKIKSVFFEYN	IREDISEYINRWPFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGDIDR	TQPIWMKYPSIFNTELSQSNIEBRYKIQSY
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	termination transports in 1944 6 . ACLES INTO	tion with a second control of the second control of		the control of the second of t
	1081 1110	1111 1140	1141 1170	1171 1200
Original_Seq42	SEYLKDFWGNPLMYNKBYYMFNAGNKNSY[]		YIGEKFIIRRKSNSQSINDDIVRKEDYIYL	DPFNLNOEWRYYTYKYPKKERE LPLAPIS
Substitute_Seq42	SEYLKDFWGNPLMYNKEYYMFNAGNKNSY	IKLKKDSPVGEILTRSKYNQNSKYINYRDL	YIGEKFIIRRKSNSQSINDDIVRKEDYIYL	DPFNLNOEWRVYTYKYFKKEEERLPLAPIS
Amended_Seq42	SEYLKDFWGNPLMYNKEYYMFNAGNKNSY	IKLKKDSPVGEILTRSKYNONSKYINYRDL	YIGEKFIIRRKSNSOSINDDIVRKRDVIVI.	DPPNI.NORWRVYTYKYPKKEEEMI.PI.ADIS
Whelan_M81186	SEYLKDFWGNPLMYNKEYYMFNAGNKNSY	IKLKKDSPVGEILTRSKYNONSKY INYRDL	YIGEKFIIRRKSNSOSINDDIVPKEDYIYI.	DPPNI.NORWRVVTVXVPKKRREMI.PI.ADIC
			***************************************	(0.00)
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Original_Seq42	DSDEFYNTIOIKEYDEOPTYSCOLLPKKDE	RSTDRIGITGINE PVESCIVERED KONDECT	SHAMI BETTER BANK AT COMPARY DADGER	TP
Substitute_Seq42	D2DELAMLIGIKEADEGBLA2COFFEKKDE	ESTDEIGLIGIHRFYESGIVFEEMKD\[PCI	SKWYLREVKRKPYNLKLGCNWOP I PKDECW	TE
Amended_Seq42				
Whelan_M81186	DSDEFINITOIKEYDEOPTYSCOLLFKKDR	RSTDRIGI.IGIHPPYRSGIVPFFMYDVPCI	CMNVI MEUROPOVIII VI COMMORTOVIOCII	AND
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